

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Lemischka, Ihor R.
- (ii) TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
RECEPTORS AND THEIR LIGANDS
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: ImClone Systems Incorporated
 - (B) STREET: 180 Varick Street
 - (C) CITY: New York
 - (D) STATE: New York
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 10014
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US UNASSIGNED
 - (B) FILING DATE: 19-NOV-1992
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US UNASSIGNED
 - (B) FILING DATE: 12-NOV-1992

- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/906,397
 - (B) FILING DATE: 26-JUN-1992
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US PCT/US92/05401
 - (B) FILING DATE: 26-JUN-1992
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: TW 81102961
 - (B) FILING DATE: 15-APR-1992
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US PCT/US92/02750
 - (B) FILING DATE: 02-APR-1992
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/813,593
 - (B) FILING DATE: 24-DEC-1991
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/793,065
 - (B) FILING DATE: 15-NOV-1991
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/728,913
 - (B) FILING DATE: 28-JUN-1991
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/679,666
 - (B) FILING DATE: 02-APR-1991
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Feit, Irving N.
 - (B) REGISTRATION NUMBER: 28,601
 - (C) REFERENCE/DOCKET NUMBER: LEM-3-7P

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 212-645-1405
- (B) TELEFAX: 212-645-2054

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 112..3006

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 31..111

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 31..3009

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCGGCCTGGC TACCGCGCGC TCCGGAGGCC ATG CGG GCG TTG GCG CAG CGC AGC	54
Met Arg Ala Leu Ala Gln Arg Ser	-20
-27 -25	
GAC CGG CGG CTG CTG CTG CTT GTT GTT TCA GTA ATG ATT CTT GAG	102
Asp Arg Arg Leu Leu Leu Val Leu Ser Val Met Ile Leu Glu	-5
-15 -10	
ACC GTT ACA AAC CAA GAC CTG CCT GTG ATC AAG TGT GTT TTA ATC AGT	150
Thr Val Thr Asn Gln Asp Leu Pro Val Ile Lys Cys Val Leu Ile Ser	10
1	
CAT GAG AAC AAT GGC TCA TCA GCG GGA AAG CCA TCA TCG TAC CGA ATG	198
His Glu Asn Asn Gly Ser Ser Ala Gly Lys Pro Ser Ser Tyr Arg Met	25
15 20	
GTG CGA GGA TCC CCA GAA GAC CTC CAG TGT ACC CCG AGG CGC CAG AGT	246
Val Arg Gly Ser Pro Glu Asp Leu Gln Cys Thr Pro Arg Arg Gln Ser	45
30 35	
GAA GGG ACG GTA TAT GAA GCG GCC ACC GTG GAG GTG GCC GAG TCT GGG	294
Glu Gly Thr Val Tyr Glu Ala Thr Val Glu Val Ala Glu Ser Gly	60
50	
TCC ATC ACC CTG CAA GTG CAG CTC GCC ACC CCA GGG GAC CTT TCC TGC	342
Ser Ile Thr Leu Gln Val Gln Leu Ala Thr Pro Gly Asp Leu Ser Cys	75
65 70	
CTC TGG GTC TTT AAG CAC AGC TCC CTG GGC TGC CAG CCG CAC TTT GAT	390
Leu Trp Val Phe Lys His Ser Ser Leu Gly Cys Gln Pro His Phe Asp	90
80 85	
TTA CAA AAC AGA GGA ATC GTT TCC ATG GCC ATC TTG AAC GTG ACA GAG	438
Leu Gln Asn Arg Gly Ile Val Ser Met Ala Ile Leu Asn Val Thr Glu	105
95 100	
	54

ACC CAG GCA GGA GAA TAC CTA CTC CAT ATT CAG AGC GAA CGC GCC AAC Thr Gln Ala Gly Glu Tyr Leu His Ile Gln Ser Glu Arg Ala Asn 110 115 120 125	486
TAC ACA GTA CTG TTC TTT ACA GTG AAT GTA AGA GAT ACA CAG CTG TAT GTG Tyr Thr Val Leu Phe Thr Val Asn Val Arg Asp Thr Gln Leu Tyr Val 130 135 140	534
CTA AGG AGA CCT TAC TTT AGG AAG ATG GAA AAC CAG GAT GCA CTG CTC Leu Arg Arg Pro Tyr Phe Arg Lys Met Glu Asn Gln Asp Ala Leu Leu 145 150 155	582
TGC ATC TCC GAG GGT GTT CCG GAG CCC ACT GTG GAG TGG GTG CTC TGC Cys Ile Ser Glu Gly Val Pro Glu Pro Thr Val Glu Trp Val Leu Cys 160 165 170	630
AGC TCC CAC AGG GAA AGC TGT AAA GAA GGC CCT GCT GTT GTC AGA Ser Ser His Arg Glu Ser Cys Lys Glu Glu Gly Pro Ala Val Val Arg 175 180 185	678
AAG GAG GAA AAG GTA CTT CAT GAG TTT GGA ACA GAC ATC AGA TGC Lys Glu Glu Lys Val Leu His Glu Leu Phe Gly Thr Asp Ile Arg Cys 190 195 200 205	726
TGT GCT AGA AAT GCA CTG GGC CGC GAA TGC ACC AAG CTG TTC ACC ATA Cys Ala Arg Asn Ala Leu Leu Arg Glu Cys Thr Lys Leu Phe Thr Ile 210 215 220	774
GAT CTA AAC CAG GCT CCT CAG AGC ACA CTG CCC CAG TTA TTC CTG AAA Asp Leu Asn Gln Ala Pro Gln Ser Thr Leu Pro Gln Leu Phe Leu Lys 225 230 235	822
GTG GGG GAA CCC TTG TGG ATC AGG TGT AAG GCC ATC CAT GTG AAC CAT Val Gly Glu Pro Leu Trp Ile Arg Cys Lys Ala Ile His Val Asn His 240 245 250	870

GGA TTC GGG CTC ACC TGG GAG CTG GAA GAC AAA GCC CTG GAG GAG GGC Gly Phe Gly Leu Thr Trp Glu Leu Glu Asp Lys Ala Leu Glu Glu Gly 255 260 265	918
AGC TAC TTT GAG ATG AGT ACC TAC TCC ACA AAC AGG ACC ATG ATT CGG Ser Tyr Phe Glu Met Ser Thr Tyr Ser Thr Asn Arg Thr Met Ile Arg 270 275 280 285	966
ATT CTC TTG GCC TTT GTG TCT TCC GTG GGA AGG AAC GAC ACC GGA TAT Ile Leu Leu Ala Phe Val Ser Ser Val Gly Arg Asn Asp Thr Gly Tyr 290 295 300	1014
TAC ACC TGC TCT TCC TCA AAG CAC CCC AGC CAG TCA GCG TTG GTG ACC Tyr Thr Cys Ser Ser Ser Lys His Pro Ser Ser Gln Ser Ala Leu Val Thr 305 310 315	1062
ATC CTA GAA AAA GGG TTT ATA AAC GCT ACC AGC TCG CAA GAA GAG TAT Ile Leu Glu Lys Gly Phe Ile Asn Ala Thr Ser Ser Gln Glu Glu Tyr 320 325 330	1110
GAA ATT GAC CCG TAC GAA AAG TTC TGC TTC TCA GTC AGG TTT AAA GCG Glu Ile Asp Pro Tyr Glu Lys Phe Cys Phe Ser Val Arg Phe Lys Ala 335 340 345	1158
TAC CCA CGA ATC CGA TGC ACG TGG ATC TTC TCT CAA GCC TCA TTT CCT Tyr Pro Arg Ile Arg Cys Thr Trp Ile Phe Ser Ser Gln Ala Ser Phe Pro 350 355 360 365	1206
TGT GAA CAG AGA GGC CTG GAG GAT GGG TAC AGC ATA TCT AAA TTT TGC Cys Glu Gln Arg Gly Leu Glu Asp Gly Tyr Ser Ile Ser Lys Phe Cys 370 375 380	1254
GAT CAT AAG AAC AAG CCA GGA GAG TAC ATA TTC TAT GCA GAA AAT GAT Asp His Lys Asn Lys Pro Gly Glu Tyr Ile Phe Tyr Ala Glu Asn Asp 385 390 395	1302

GAC GCC CAG TTC ACC AAA ATG TTC ACG CTG AAT ATA AGA AAG AAA CCT Asp Ala Gln Phe Thr Lys Met 405 400	1350
CAA GTG CTA GCA AAT GCC TCA GCC AGC CAG GCG TCC TGT TCC TCT GAT Gln Val Leu Ala Asn Ala 420 415	1398
GGC TAC CCG CTA CCC TCT TGG ACC TGG AAG AAG TGT TCG GAC AAA TCT Gly Tyr Pro Leu Pro Ser Trp Thr Trp Lys 440 435	1446
CCC AAT TGC ACG GAG GAA ATC CCA GAA GGA GTT TGG AAT AAA AAG GCT Pro Asn Cys Thr Glu Glu Ile Pro Glu 455 450	1494
AAC AGA AAA GTG TTT GGC CAG TGG GTG TCG AGC AGT ACT CTA AAT ATG Asn Arg Lys Val Phe 465 460	1542
AGT GAG GCC GGG AAA GGG CTT CTG GTC AAA TGC TGT GCG TAC AAT TCT Ser Glu Ala Glu Lys Lys Glu Leu Val 485 480	1590
ATG GGC ACG TCT TGC GAA ACC ATC TTT TTA AAC TCA CCA GGC CCC TTC Met Gly Thr Ser Cys Glu Thr 500 495	1638
CCT TTC ATC CAA GAC AAC ATC TCC TTC TAT GCG ACC ATT GGG CTC TGT Pro Phe Ile Gln Asp Asn Ile Ser Phe Tyr Ala Thr 520 515	1686
CTC CCC TTC ATT GTT GTT CTC ATC GTG TTG ATC TGC CAC AAA TAC AAA Leu Pro Phe Ile Val Val Leu Ile Val 535 530	1734

AAG CAA TTT AGG TAC GAG AGT CAG CTG CAG ATG ATC CAG GTG ACT GGC Lys Gln Phe Arg Tyr Glu Ser Gln Leu Gln Met Ile Gln Val Thr Gly	1782
CCC CTG GAT AAC GAG TAC TTC TAC GTT GAC TTC AGG GAC TAT GAA TAT Pro Leu Asp Asn Glu Tyr Phe Tyr Val Asp Phe Arg Asp Tyr Glu Tyr	1830
GAC CTT AAG TGG GAG TTC CCG AGA GAG AAC TTA GAG TTT GGG AAG GTC Asp Leu Lys Trp Glu Phe Pro Arg Glu Asn Leu Glu Phe Gly Lys Val	1878
CTG GGG TCT GGC GCT TTC GGG AGG AGG GTG ATG AAC GCC ACG GCC TAT GGC Leu Gly Ser Gly Ala Phe Gly Arg Val Met Asn Ala Thr Ala Tyr Gly	1926
ATT AGT AAA ACG GGA GTC TCA ATT CAG GTG GCG ATG AAG AAG ATG CTA AAA Ile Ser Lys Thr Gly Val Ser Ile Gln Val Ala Val Lys Met Leu Lys	1974
GAG AAA GCT GAC AGC TGT GAA AAA GAA GCT CTC ATG TCG GAG CTC AAA Glu Lys Ala Asp Ser Cys Glu Lys Glu Ala Leu Met Ser Glu Leu Lys	2022
ATG ATG ACC CAC CTG GGA CAC CAT GAC AAC ATC GTG AAT CTG CTG GGG Met Met Thr His Leu Gly His His Asp Asn Ile Val Asn Leu Leu Gly	2070
GCA TGC ACA CTG TCA GGG CCA GTG TAC TTG ATT TTT GAA TAT TGT TGC Ala Cys Thr Leu Ser Gly Pro Val Tyr Leu Ile Phe Glu Tyr Cys Cys	2118
TAT GGT GAC CTC AAC TAC CTA AGA AGT AAA AGA GAG AAG TTT CAC Tyr Gly Asp Leu Leu Asn Tyr Leu Arg Ser Lys Arg Glu Lys Phe His	2166

AGG ACA TGG ACA GAG ATT TTT AAG GAA CAT AAT TTC AGT TCT TAC CCT Arg Thr Trp Thr Glu Ile Phe Lys Glu His Asn Phe Ser Tyr Pro 690 695 700	2214
ACT TTC CAG GCA CAT TCA AAT TCC AGC ATG CCT GGT TCA CGA GAA GTT Thr Phe Gln Ala His Ser Asn Ser Met Pro Gly Ser Arg Glu Val 705 710 715	2262
CAG TTA CAC CCG CCC TTG GAT CAG CTC TCA GGG TTC AAT GGG AAT TCA Gln Leu His Pro Pro Leu Asp Gln Leu Ser Ser Gly Phe Asn Gly Asn Ser 720 725 730	2310
ATT CAT TCT GAA GAT GAG ATT GAA TAT GAA AAC CAG AAG AGG CTG GCA Ile His Ser Glu Asp Glu Ile Glu Tyr Glu Asn Gln Lys Arg Leu Ala 735 740 745	2358
GAA GAA GAG GAG GAT TTG AAC GTG CTG ACG TTT GAA GAC CTC CTT Glu Glu Glu Glu Asp Leu Asn Val Leu Thr Phe Glu Asp Leu Leu 750 755 760 765	2406
TGC TTT GCG TAC CAA GTG GCC AAA GGC ATG GAA TTC CTG GAG TTC AAG Cys Phe Ala Tyr Gln Val Ala Lys Gly Met Glu Phe Leu Glu Phe Lys 770 775 780	2454
TCG TGT GTC CAC AGA GAC CTG GCA GCC AGG AAT GTG TTG GTC ACC CAC Ser Cys Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Thr His 785 790 795	2502
GGG AAG GTG GTG AAG ATC TGT GAC TTT GGA CTG GCC CGA GAC ATC CTG Gly Lys Val Val Lys Ile Cys Asp Phe Gly Leu Ala Arg Asp Ile Leu 800 805 810	2550
AGC GAC TCC AGC TAC GTC GTC AGG GGC AAC GCA CGG CTG CCG GTG AAG Ser Asp Ser Ser Tyr Val Val Arg Gly Asn Ala Arg Leu Pro Val Lys 815 820 825	2598

TGG ATG GCA CCC GAG AGC TTA TTT GAA GGG ATC TAC ACA ATC AAG AGT 2646
 Trp Met Ala Pro Glu Ser Leu Phe Glu Gly Ile Tyr Thr Ile Lys Ser 845
 830
 GAC GTC TGG TCC TAC GGC ATC CTT CTC TGG GAG ATA TTT TCA CTG GGT 2694
 Asp Val Trp Ser Tyr Gly Ile Leu Leu Trp Glu Ile Phe Ser Leu Gly 860
 850
 GTG AAC CCT TAC CCT GGC ATT CCT GTC GAC GCT AAC TTC TAT AAA CTG 2742
 Val Asn Pro Tyr Pro Gly Ile Ile Pro Val Asp Ala Asn Phe Tyr Lys Leu 875
 865
 ATT CAG AGT GGA TTT AAA ATG GAG CAG CCA TTC TAT GCC ACA GAA GGG 2790
 Ile Gln Ser Gly Phe Lys Met Glu Gln Pro Phe Tyr Ala Thr Glu Gly 890
 880
 ATA TAC TTT GTA ATG CAA TCC TGC TGG GCT TTT GAC TCA AGG AAG CGG 2838
 Ile Tyr Phe Val Met Gln Ser Cys Trp Ala Phe Asp Ser Arg Lys Arg 905
 895
 CCA TCC TTC CCC AAC CTG ACT TCA TTT TTA GGA TGT CAG CTG GCA GAG 2886
 Pro Ser Phe Pro Asn Leu Thr Ser Phe Leu Gly Cys Gln Leu Ala Glu 925
 910
 GCA GAA GAA GCA TGT ATC AGA ACA TCC ATC CAT CTA CCA AAA CAG GCG 2934
 Ala Glu Glu Ala Cys Ile Arg Thr Ser Ile His Leu Pro Lys Gln Ala 940
 930
 GCC CCT CAG CAG AGA GGC GGC CTC AGA GCC CAG TCG CCA CAG CGC CAG 2982
 Ala Pro Gln Gln Arg Gly Gly Leu Arg Ala Gln Ser Pro Gln Arg Gln 955
 945
 GTG AAG ATT CAC AGA GAA AGA AGT TAGCGAGGAG GCCTTGGACC CCGCCACCCT 3036
 Val Lys Ile His Arg Glu Arg Ser 965
 960
 AGCAGGCTGT AGACCGCAGA GCCAAGATTA GCCTCGCCTC TGAGGAAGCG CCCTACAGCG 3096

CGTTGCTTCG	CTGGACTTTT	CTCTAGATGC	TGTCTGCCAT	TACTCCAAAG	TGACTTCTAT	3156
AAAATCAAAC	CTCTCCTCGC	ACAGCGCGGA	GAGCCAATAA	TGAGACTTGT	TGGTGAGCCC	3216
GCCTACCCCTG	GGGGCCCTTC	CACGAGCTTG	AGGGGAAAGC	CATGTATCTG	AAATATAGTA	3276
TATTC TTGTA	AATACGTGAA	ACAAACCAAA	CCCGTTT TTT	GCTAAGGGAA	AGCTAAATAT	3336
GATTTT TAAA	AATCTATGTT	TTAAATAACT	ATGTAAC TTT	TTCATCTATT	TAGTGATATA	3396
TTTTATGGAT	GGAAATAAAC	TTTCTACTGT	AAAAAAAAAA	AAAAAAAAAA	AAAAAAA	3453

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 992 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Arg	Ala	Leu	Ala	Gln	Arg	Ser	Asp	Arg	Leu	Leu	Leu	Val	
-27	-25					-20				-15				
Val	Leu	Ser	Val	Met	Ile	Leu	Glu	Thr	Val	Thr	Asn	Gln	Asp	Leu
	-10				-5					1				5
Val	Ile	Lys	Cys	Val	Leu	Ile	Ser	His	Glu	Asn	Asn	Gly	Ser	Ser
			10						15				20	
Gly	Lys	Pro	Ser	Ser	Tyr	Arg	Met	Val	Arg	Gly	Ser	Pro	Glu	Asp
			25				30						35	Leu

TABLE "B" CONTINUED

Gln Cys	Thr	Pro	Arg	Arg	Gln	Ser	Glu	Gly	Thr	Val	Tyr	Glu	Ala	Ala	
	40					45					50				
Thr	Val	Glu	Val	Ala	Glu	Ser	Gly	Ser	Ile	Thr	Leu	Gln	Val	Gln	Leu
	55					60					65				
Ala	Thr	Pro	Gly	Asp	Leu	Ser	Cys	Leu	Trp	Val	Phe	Lys	His	Ser	Ser
	70					75				80					85
Leu	Gly	Cys	Gln	Pro	His	Phe	Asp	Leu	Gln	Asn	Arg	Gly	Ile	Val	Ser
					90				95						100
Met	Ala	Ile	Leu	Asn	Val	Thr	Glu	Thr	Gln	Ala	Gly	Glu	Tyr	Leu	Leu
			105				110							115	
His	Ile	Gln	Ser	Glu	Arg	Ala	Asn	Tyr	Thr	Val	Leu	Phe	Thr	Val	Asn
			120				125					130			
Val	Arg	Asp	Thr	Gln	Leu	Tyr	Val	Leu	Arg	Arg	Pro	Tyr	Phe	Arg	Lys
			135			140					145				
Met	Glu	Asn	Gln	Asp	Ala	Leu	Leu	Cys	Ile	Ser	Glu	Gly	Val	Pro	Glu
	150					155				160					165
Pro	Thr	Val	Glu	Trp	Val	Leu	Cys	Ser	Ser	His	Arg	Glu	Ser	Cys	Lys
					170					175				180	
Glu	Glu	Gly	Pro	Ala	Val	Val	Arg	Lys	Glu	Glu	Lys	Val	Leu	His	Glu
			185					190					195		
Leu	Phe	Gly	Thr	Asp	Ile	Arg	Cys	Cys	Ala	Arg	Asn	Ala	Leu	Gly	Arg
			200				205					210			
Glu	Cys	Thr	Lys	Leu	Phe	Thr	Ile	Asp	Leu	Asn	Gln	Ala	Pro	Gln	Ser
						220					225				

Thr	Leu	Pro	Gln	Leu	Phe	Leu	Lys	Val	Gly	Glu	Pro	Leu	Trp	Ile	Arg
230					235				240						245
Cys	Lys	Ala	Ile	His	Val	Asn	His	Gly	Phe	Gly	Leu	Thr	Trp	Glu	Leu
				250				255						260	
Glu	Asp	Lys	Ala	Leu	Glu	Glu	Gly	Ser	Tyr	Phe	Glu	Met	Ser	Thr	Tyr
			265					270					275		
Ser	Thr	Asn	Arg	Thr	Met	Ile	Arg	Ile	Leu	Leu	Ala	Phe	Val	Ser	Ser
			280				285					290			
Val	Gly	Arg	Asn	Asp	Thr	Gly	Tyr	Tyr	Thr	Cys	Ser	Ser	Ser	Lys	His
						300					305				
Pro	Ser	Gln	Ser	Ala	Leu	Val	Thr	Ile	Leu	Glu	Lys	Gly	Phe	Ile	Asn
310					315					320					325
Ala	Thr	Ser	Ser	Gln	Glu	Glu	Tyr	Glu	Ile	Asp	Pro	Tyr	Glu	Lys	Phe
				330					335					340	
Cys	Phe	Ser	Val	Arg	Phe	Lys	Ala	Tyr	Pro	Arg	Ile	Arg	Cys	Thr	Trp
			345					350					355		
Ile	Phe	Ser	Gln	Ala	Ser	Phe	Pro	Cys	Glu	Gln	Arg	Gly	Leu	Glu	Asp
			360				365					370			
Gly	Tyr	Ser	Ile	Ser	Lys	Phe	Cys	Asp	His	Lys	Asn	Lys	Pro	Gly	Glu
						380					385				
Tyr	Ile	Phe	Tyr	Ala	Glu	Asn	Asp	Asp	Ala	Gln	Phe	Thr	Lys	Met	Phe
390					395					400					405
Thr	Leu	Asn	Ile	Arg	Lys	Lys	Pro	Gln	Val	Leu	Ala	Asn	Ala	Ser	Ala
									415						

Ser Gln Ala Ser Cys Ser Ser Asp Gly Tyr Pro Leu Pro Ser Trp Thr
 425 430 435
 Trp Lys Lys Cys Ser Asp Lys Ser Pro Asn Cys Thr Glu Glu Ile Pro
 440 445 450
 Glu Gly Val Trp Asn Lys Lys Ala Asn Arg Lys Val Phe Gly Gln Trp
 455 460 465
 Val Ser Ser Thr Leu Asn Met Ser Glu Ala Gly Lys Gly Leu Leu
 470 475 480 485
 Val Lys Cys Cys Ala Tyr Asn Ser Met Gly Thr Ser Cys Glu Thr Ile
 490 495 500
 Phe Leu Asn Ser Pro Gly Pro Phe Ile Gln Asp Asn Ile Ser
 505 510 515
 Phe Tyr Ala Thr Ile Gly Leu Cys Leu Pro Phe Ile Val Val Leu Ile
 520 525 530
 Val Leu Ile Cys His Lys Tyr Lys Lys Gln Phe Arg Tyr Glu Ser Gln
 535 540 545
 Leu Gln Met Ile Gln Val Thr Gly Pro Leu Asp Asn Glu Tyr Phe Tyr
 550 555 560 565
 Val Asp Phe Arg Asp Tyr Glu Tyr Asp Leu Lys Trp Glu Phe Pro Arg
 570 575 580
 Glu Asn Leu Glu Phe Gly Lys Val Leu Gly Ser Gly Ala Phe Gly Arg
 585 590 595
 Val Met Asn Ala Thr Ala Tyr Gly Ile Ser Lys Thr Gly Val Ser Ile
 600 605 610

Gln Val Ala Val Lys Met Leu Lys Glu Lys Ala Asp Ser Cys Glu Lys
615 620 625

Glu Ala Leu Met Ser Glu Leu Lys Met Met Thr His Leu Gly His His
630 635 640 645

Asp Asn Ile Val Asn Leu Leu Gly Ala Cys Thr Leu Ser Gly Pro Val
650 655 660

Tyr Leu Ile Phe Glu Tyr Cys Cys Tyr Gly Asp Leu Leu Asn Tyr Leu
665 670 675

Arg Ser Lys Arg Glu Lys Phe His Arg Thr Trp Thr Glu Ile Phe Lys
680 685 690

Glu His Asn Phe Ser Ser Tyr Pro Thr Phe Gln Ala His Ser Asn Ser
695 700 705

Ser Met Pro Gly Ser Arg Glu Val Gln Leu His Pro Pro Leu Asp Gln
710 715 720 725

Leu Ser Gly Phe Asn Gly Asn Ser Ile His Ser Glu Asp Glu Ile Glu
730 735 740

Tyr Glu Asn Gln Lys Arg Leu Leu Ala Glu Glu Glu Glu Asp Leu Asn
745 750 755

Val Leu Thr Phe Glu Asp Leu Leu Cys Phe Ala Tyr Gln Val Ala Lys
760 765 770

Gly Met Glu Phe Leu Glu Phe Lys Ser Cys Val His Arg Asp Leu Ala
775 780 785

Ala Arg Asn Val Leu Val Thr His Gly Lys Val Val Lys Ile Cys Asp
790 795 800 805

Phe Gly Leu Ala Arg Asp Ile Leu Ser Asp Ser Tyr Val Val Arg
 810 815 820
 Gly Asn Ala Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ser Leu Phe
 825 830 835
 Glu Gly Ile Tyr Thr Ile Lys Ser Asp Val Trp Ser Tyr Gly Ile Leu
 840 845 850
 Leu Trp Glu Ile Phe Ser Leu Gly Val Asn Pro Tyr Pro Gly Ile Pro
 855 860 865
 Val Asp Ala Asn Phe Tyr Lys Leu Ile Gln Ser Gly Phe Lys Met Glu
 870 875 880 885
 Gln Pro Phe Tyr Ala Thr Glu Gly Ile Tyr Phe Val Met Gln Ser Cys
 890 895 900
 Trp Ala Phe Asp Ser Arg Lys Arg Pro Ser Phe Pro Asn Leu Thr Ser
 905 910 915
 Phe Leu Gly Cys Gln Leu Ala Glu Ala Glu Glu Ala Cys Ile Arg Thr
 920 925 930
 Ser Ile His Leu Pro Lys Gln Ala Ala Pro Gln Gln Arg Gly Gly Leu
 935 940 945
 Arg Ala Gln Ser Pro Gln Arg Gln Val Lys Ile His Arg Glu Arg Ser
 950 955 960 965

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3501 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 58..3039

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 139..3036

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 58..138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGAGCGGCA	TCCGAGGGCT	GGCGGGCGC	CCTGGGGAC	CCCGGGCTCC	GGAGGCC	57
ATG CCG GCG TTG GCG GAC GCG GGC ACC GTG CCG CTG CTC GTT GTT						105
Met Pro Ala Leu Ala Arg Asp Ala Gly Thr Val Pro Leu Leu Val Val						
-27 -25			-20		-15	
TTT TCT GCA ATG ATA TTT GGG ACT ATT ACA AAT CAA GAT CTG CCT GTG						153
Phe Ser Ala Met Ile Phe Gly Thr Ile Thr Asn Gln Asp Leu Pro Val						
-10			-5		1 5	

ATC AAG TGT GTT TTA ATC AAT CAT AAG AAC AAT GAT TCA TCA GTG GGG Ile Lys Cys Val Leu 10 15	201
AAG TCA TCA TCA TAT CCC ATG GTA TCA GAA TCC CCG GAA GAC CTC GGG Lys Ser Ser Tyr Pro Met Val Ser Glu Ser Pro Glu Asp Leu Gly 35 25	249
TGT GCG TTG AGA CCC CAG AGC TCA GGG ACA GTG TAC GAA GCT GCC GCT Cys Ala Leu Arg Pro Gln Ser Ser Glu Thr Val Tyr Glu Ala Ala 50 40	297
GTG GAA GTG GAT GTA TCT GCT TCC ATC ACA CTG CAA GTG CTG GTC GAT Val Glu Val Asp Val Ser Ala Ser Ile Thr Leu Gln Val Leu Val Asp 65 55	345
GCC CCA GGG AAC ATT TCC TCT GTC TTT AAG CAC AGC TCC CTG Ala Pro Gly Asn Ile Ser Cys Leu Trp Val Phe Lys His Ser Ser Leu 85 70	393
AAT TGC CAG CCA CAT TTT GAT TTA CAA AAC AGA GGA GTT GTT TCC ATG Asn Cys Gln Pro His Phe Asp Leu Gln Asn Arg Gly Val Val Ser Met 100 90	441
GTC ATT TTG AAA ATG ACA ACC CAA GCT GGA GAA TAC CTA CTT TTT Val Ile Leu Lys Met Thr Glu Thr Gln Ala Gly Glu Tyr Leu Leu Phe 115 105	489
ATT CAG AGT GAA GCT ACC AAT TAC ACA ATA TTG TTT ACA GTG AGT ATA Ile Gln Ser Glu Ala Thr Asn Tyr Thr Ile Leu Phe Thr Val Ser Ile 130 120	537
AGA AAT ACC CTG CTT TAC ACA TTA AGA AGA CCT TAC TTT AGA AAA ATG Arg Asn Thr Leu Leu Tyr Thr Leu Arg Arg Pro Tyr Phe Arg Lys Met 145 135	585

GAA AAC CAG GAC GCC CTG GTC TGC ATA TCT GAG AGC GTT CCA GAG CCG Glu Asn Gln Asp Ala Leu Val Cys Ile Ser Glu Ser Val Pro Glu Pro 150 155 160 165	633
ATC GTG GAA TGG GTG CTT TGC GAT TCA CAG GGG GAA AGC TGT AAA GAA Ile Val Glu Trp Val Leu Cys Asp Ser Gln Gly Glu Ser Cys Lys Glu 170 175 180	681
GAA AGT CCA GCT GTT GTT AAA AAG GAG GAA AAA GTG CTT CAT GAA TTA Glu Ser Pro Ala Val Val Lys Lys Glu Glu Lys Val Leu His Glu Leu 185 190 195	729
TTT GGG ACG GAC ATA AGG TGC TGT GCC AGA AAT GAA CTG GGC AGG GAA Phe Gly Thr Arg Leu Ile Arg Cys Cys Ala Arg Asn Glu Leu Gly Arg Glu 200 205 210	777
TGC ACC AGG CTG TTC ACA ATA GAT CTA AAT CAA ACT CCT CAG ACC ACA Cys Thr Arg Leu Phe Thr Ile Asp Leu Asn Gln Thr Pro Gln Thr Thr 215 220 225	825
TTG CCA CAA TTA TTT CTT AAA GTA GGG GAA CCC TTA TGG ATA AGG TGC Leu Pro Gln Leu Phe Leu Lys Val Gly Glu Pro Leu Trp Ile Arg Cys 230 235 240 245	873
AAA GCT GTT CAT GTG AAC CAT GGA TTC GGG CTC ACC TGG GAA TTA GAA Lys Ala Val His Val Asn His Gly Phe Gly Leu Thr Trp Glu Leu Glu 250 255 260	921
AAC AAA GCA CTC GAG GAG GGC AAC TAC TTT GAG ATG AGT ACC TAT TCA Asn Lys Ala Leu Glu Glu Gly Asn Tyr Phe Glu Met Ser Thr Tyr Ser 265 270 275	969
ACA AAC AGA ACT ATG ATA CGG ATT CTG TTT GCT TTT GTA TCA TCA GTG Thr Asn Arg Thr Met Ile Arg Ile Leu Phe Ala Phe Val Ser Ser Val 280 285 290	1017

GCA AGA AAC GAC ACC GGA TAC TAC ACT TGT TCC TCT TCA AAG CAT CCC Ala Arg Asn Asp Thr Gly 300 Tyr Tyr Thr Cys Ser 305 TCA AAG CAT CCC 295	1065
AGT CAA TCA GCT TTG GTT ACC ATC GTA GGA AAG GGA TTT ATA AAT GCT Ser Gln Ser Ala Leu Val 315 Thr Ile Val Gly Lys Gly Phe Ile Asn Ala 310	1113
ACC AAT TCA AGT GAA GAT TAT GAA ATT GAC CAA TAT GAA GAG TTT TGT Thr Asn Ser Ser Glu Asp Tyr Glu Ile 330 Asp Gln Tyr Glu Glu Phe Cys 335	1161
TTT TCT GTC AGG TTT AAA GCC TAC CCA CAA AAG GGT CTT GAT AAC GGA Phe Ser Val Arg 345 Phe Lys Ala Tyr Pro Gln Ile Arg Cys Thr Trp Thr 350	1209
TTC TCT CGA AAA TCA TTT CCT TGT GAG CAA AAG GGT CTT GAT AAC GGA Phe Ser Arg Lys Ser Phe 360 Pro Cys Glu Gln Lys Gly Leu Asp Asn Gly 370	1257
TAC AGC ATA TCC AAG TTT TGC AAT CAT AAG CAC CAG CCA GGA GAA TAT Tyr Ser Ile Ser Lys Phe 380 Cys Asn His Lys His Gln Pro Gly Glu Tyr 385	1305
ATA TTC CAT GCA GAA AAT GAT GAT GCC CAA TTT ACC AAA ATG TTC ACG Ile Phe His Ala Glu 395 Asn Asp Asp Ala Gln Phe Thr Lys Met Phe Thr 400	1353
CTG AAT ATA AGA AGG AAA CCT CAA GTG CTC GCA GAA GCA TCG GCA AGT Leu Asn Ile Arg Arg Lys 410 Pro Gln Val Leu Ala Glu Ala Ser Ala Ser 420	1401
CAG GCG TCC TGT TTC TCG GAT GGA TAC CCA TTA CCA TCT TGG ACC TGG Gln Ala Ser Cys Phe 425 Thr Ser Asp Gly Tyr Pro Leu Pro Ser Trp Thr Trp 435	1449

AAG AAG TGT TCA GAC AAG AAG TCT CCC AAC TGC ACA GAA GAG ATC ACA GAA Lys Lys Cys Ser Asp Lys Ser 445 440	1497
GGA GTC TGG AAT AGA AAG AAG GCT AAC AGA AAA GTG TTT GGA CAG TGG GTG Gly Val Trp Asn Arg Lys Ala Asn Arg Lys Val Phe Gly Gln Trp Val 455 460	1545
TCG AGC AGT ACT CTA AAC AAG ATG AGT GAA GCC ATA AAA GGG TTC CTG GTC Ser Ser Ser Thr Leu Asn Met Ser Ser Glu Ala Ile Lys Gly Phe Leu Val 470 475	1593
AAG TGC TGT GCA TAC AAT TCC CTT GGC ACA TCT TGT GAG ACG ATC CTT Lys Cys Cys Ala Tyr Asn Ser Leu Gly Thr Ser Cys Glu Thr Ile Leu 490 495	1641
TTA AAC TCT CCA GGC CCC TTC CCT TTC ATC CAA GAC AAC ATC TCA TTC Leu Asn Ser Pro Gly Pro Phe Pro Phe Ile Gln Asp Asn Ile Ser Phe 505 510	1689
TAT GCA ACA ATT GGT GTT TGT CTC CTC TTC ATT GTC GTT TTA ACC CTG Tyr Ala Thr Ile Gly Val Cys Leu Leu Phe Ile Val Val Leu Thr Leu 520 525	1737
CTA ATT TGT CAC AAG TAC AAA AAG CAA TTT AGG TAT GAA AGC CAG CTA Leu Ile Cys His Lys Tyr Lys Lys Gln Phe Arg Tyr Glu Ser Gln Leu 535 540	1785
CAG ATG GTA CAG GTG ACC GGC TCC TCA GAT AAT GAG TAC TTC TAC GTT Gln Met Val Gln Val Thr Gly Ser Ser Asp Asn Asn Glu Tyr Phe Tyr Val 550 555	1833
GAT TTC AGA GAA TAT GAA TAT GAT CTC AAA TGG GAG TTT CCA AGA GAA Asp Phe Arg Glu Tyr Glu Tyr Asp Leu Lys Trp Glu Phe Pro Arg Glu 570 575	1881

[illegible]

1929	AAATTTTGGGAGGATGGA	CTATGGA	GGTGGT	TCTTTGGA	AAA	GTG
	AsnLeuGlu	PheGlyLysVal	GlyLysVal	AlaSerGly	PheGlyLys	Val
	585		590		595	
1977	ATGAAACGCAACA	GCTTATGGA	ATTTAGC	AAAACA	GGA	ATC
	MetAsnAla	ThrAlaTyrGly	IleSerGly	LysThr	ValSer	Gln
	600	605	610			
2025	GTTGCCGTC	AAATGCTG	AAAGAA	GACAGC	TCTGAA	AGA
	ValAlaAla	LysMetLeu	LysGlu	AspSer	GluArg	Glu
	615	620	625			
2073	GCACTCATG	TCAAAATG	CTCCTG	ACCAGC	CTGGAG	CAC
	AlaLeuMet	SerGluLeu	MetMet	ThrGln	SerHis	Glu
	630	635	640			645
2121	AATATTGTG	AACCTG	GGGCTG	ACATG	GGA	TAC
	AsnIleVal	AsnLeuLeu	AlaGly	ThrLeu	ProIle	Tyr
		650	655		660	
2169	TTGATT	GAA	TACTGT	GATCTT	AAC	AGA
	LeuIlePhe	GluTyrCys	TyrCys	LeuLeu	TyrLeu	Arg
	665	670			675	
2217	AGTAAAGA	GAAGG	ACTAGG	ACATG	ATTTTC	GAA
	SerLysArg	GluLysPhe	ThrArg	ThrThr	IlePhe	Glu
	680	685			690	
2265	CACAAT	TTCAGT	TTT	CACTTC	CAATTC	AGC
	HisAsnPhe	SerPheTyr	ProThrPhe	HisSer	AsnSer	Ser
	695	700		705		
2313	ATGCCT	GGTTCA	GAAGTT	CACATA	GATGAT	ATC
	MetProGly	SerArgGlu	ValGlnIle	HisPro	AspSer	Ile
	710	715	720			725

TCA GGG CTT CAT GGG AAT TCA TTT CAC TCT GAA GAT GAA ATT GAA TAT Ser Gly Leu His Gly Asn Ser Phe His Ser Glu Asp Glu Ile Glu Tyr 730 735 740	2361
GAA AAC CAA AAA AGG CTG GAA GAA GAG GAC TTG AAT GTG CTT ACA Glu Asn Gln Lys Arg Leu Glu Glu Glu Asp Leu Asn Val Leu Thr 745 750 755	2409
TTT GAA GAT CTT CTT TGC TTT GCA TAT CAA GTT GCC AAA GGA ATG GAA Phe Glu Asp Leu Leu Cys Phe Ala Tyr Gln Val Ala Lys Gly Met Glu 760 765 770	2457
TTT CTG GAA TTT AAG TCG TGT GTT CAC AGA GAC CTG GCC GCC AGG AAC Phe Leu Glu Phe Lys Ser Cys Val His Arg Asp Leu Ala Ala Arg Asn 775 780 785	2505
GTG CTT GTC ACC CAC GGG AAA GTG GTG AAG ATA TGT GAC TTT GGA TTG Val Leu Val Thr His Gly Lys Val Val Lys Ile Cys Asp Phe Gly Leu 790 795 800 805	2553
GCT CGA GAT ATC ATG AGT GAT TCC AAC TAT GTT GTC AGG GGC AAT GCC Ala Arg Asp Ile Met Ser Ser Asp Ser Asn Tyr Val Val Arg Gly Asn Ala 810 815 820	2601
CGT CTG CCT GTA AAA TGG ATG GCC CCC GAA AGC CTG TTT GAA GGC ATC Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ser Leu Phe Glu Gly Ile 825 830 835	2649
TAC ACC ATT AAG AGT GAT GTC TGG TCA TAT GGA ATA TTA CTG TGG GAA Tyr Thr Ile Lys Ser Asp Val Trp Ser Tyr Gly Ile Leu Leu Trp Glu 840 845 850	2697
ATC TTC TCA CTT GGT GTG AAT CCT TAC CCT GGC ATT CCG GTT GAT GCT Ile Phe Ser Leu Gly Val Asn Pro Tyr Pro Gly Ile Pro Val Asp Ala 855 860 865	2745

AAC TTC TAC AAA CTG ATT CAA AAT GGA TTT AAA ATG GAT CAG CCA TTT 2793
Asn Phe Tyr Lys Leu Ile Gln Asn Gly Phe Lys Met Asp Gln Pro Phe
870 875 880 885
TAT GCT ACA GAA GAA ATA TAC ATT ATA ATG CAA TCC TGC TGG GCT TTT 2841
Tyr Ala Thr Glu Glu Ile Tyr Ile Ile Met Gln Ser Cys Trp Ala Phe
890 895 900
GAC TCA AGG AAA CGG CCA TCC TTC CCT AAT TTG ACT TCG TTT TTA GGA 2889
Asp Ser Arg Lys Arg Pro Ser Phe Pro Asn Leu Thr Ser Phe Leu Gly
905 910 915
TGT CAG CTG GCA GAT GCA GAA GAA GCG ATG TAT CAG AAT GTG GAT GGC 2937
Cys Gln Leu Ala Asp Ala Glu Glu Ala Met Tyr Gln Asn Val Asp Gly
920 925 930
CGT GTT TCG GAA TGT CCT CAC ACC TAC CAA AAC AGG CGA CCT TTC AGC 2985
Arg Val Ser Glu Cys Pro His Thr Tyr Gln Asn Arg Arg Pro Phe Ser
935 940 945
AGA GAG ATG GAT TTG GGG CTA CTC TCT CCG CAG GCT CAG GTC GAA GAT 3033
Arg Glu Met Asp Leu Gly Leu Ser Pro Gln Ala Gln Val Glu Asp
950 955 960
TCG TAGAGGAACA ATT TAG TTTT AAGGACTTCA TCCCTCCACC TATCCCTAAC 3086
Ser
AGGCTGTAGA TTACCAAAAC AAGATTAAAT TCATCACTAA AAGAAAAATCT ATTATCAACT 3146
GCTGCTTCAC CAGACTTTTC TCTAGAAAGCC GTCTGCGTTT ACTCTTGTTT TCAAAGGGAC 3206
TTTTTGTAATA TCAAATCATC CTGTCACAAG GCAGGAGGAG CTGATAAATGA ACTTTATTGG 3266
AGCATTGATC TGCATCCAAG GCCTTCTCAG GCCGGCTTGA GTGAATTGTG TACCTGAAGT 3326
ACAGTATATT CTTGTAAATA CATAAAACAA AAGCATTTTG CTAAGGAGAA GCTAATATGA 3386

TTTTTTTAAGT CTATGTGTTTA AAATAATATG TAAATTTTTC AGCTATTTAG TGATATATTT 3446
 TATGGGTGGG AATAAAATTT CTAACACAGA AAAAAAAAAA AAAAAAAAAA AAAAA 3501

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 993 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Pro	Ala	Leu	Ala	Arg	Asp	Ala	Gly	Thr	Val	Pro	Leu	Leu	Val	Val	-27	-25	-20	-15
Phe	Ser	Ala	Met	Ile	Phe	Gly	Thr	Ile	Thr	Asn	Gln	Asp	Leu	Pro	Val	-10	-5	1	5
Ile	Lys	Cys	Val	Leu	Ile	Asn	His	Lys	Asn	Asn	Asp	Ser	Ser	Val	Gly	10	15	20	
Lys	Ser	Ser	Tyr	Pro	Met	Val	Ser	Glu	Ser	Pro	Glu	Asp	Leu	Gly		25	30	35	
Cys	Ala	Leu	Arg	Pro	Gln	Ser	Ser	Gly	Thr	Val	Tyr	Glu	Ala	Ala	Ala	40	45	50	
Val	Glu	Val	Asp	Val	Ser	Ala	Ser	Ile	Thr	Leu	Gln	Val	Leu	Val	Asp	55	60	65	
Ala	Pro	Gly	Asn	Ile	Ser	Cys	Leu	Trp	Val	Phe	Lys	His	Ser	Ser	Leu	70	75	80	85

Asn Cys Gln Pro His Phe Asp Leu Gln Asn Arg Gly Val Val Ser Met
 90 95 100
 Val Ile Leu Lys Met Thr Glu Thr Gln Ala Gly Glu Tyr Leu Leu Phe
 105 110 115
 Ile Gln Ser Glu Ala Thr Asn Tyr Thr Ile Leu Phe Thr Val Ser Ile
 120 125 130
 Arg Asn Thr Leu Leu Tyr Thr Leu Arg Arg Pro Tyr Phe Arg Lys Met
 135 140 145
 Glu Asn Gln Asp Ala Leu Val Cys Ile Ser Glu Ser Val Pro Glu Pro
 150 155 160 165
 Ile Val Glu Trp Val Leu Cys Asp Ser Gln Gly Glu Ser Cys Lys Glu
 170 175 180
 Glu Ser Pro Ala Val Val Lys Lys Glu Glu Lys Val Leu His Glu Leu
 185 190 195
 Phe Gly Thr Asp Ile Arg Cys Cys Ala Arg Asn Glu Leu Gly Arg Glu
 200 205 210
 Cys Thr Arg Leu Phe Thr Ile Asp Leu Asn Gln Thr Pro Gln Thr Thr
 215 220 225
 Leu Pro Gln Leu Phe Leu Lys Val Gly Glu Pro Leu Trp Ile Arg Cys
 230 235 240 245
 Lys Ala Val His Val Asn His Gly Phe Gly Leu Thr Trp Glu Leu Glu
 250 255 260
 Asn Lys Ala Leu Glu Glu Gly Asn Tyr Phe Glu Met Ser Thr Tyr Ser
 265 270 275

Thr Asn Arg Thr Met Ile Arg Ile Leu Phe Ala Phe Val Ser Ser Val
 280 285 290
 Ala Arg Asn Asp Thr Gly Tyr Tyr Thr Cys Ser Ser Ser Lys His Pro
 295 300 305
 Ser Gln Ser Ala Leu Val Thr Ile Val Gly Lys Gly Phe Ile Asn Ala
 310 315 320 325
 Thr Asn Ser Ser Glu Asp Tyr Glu Ile Asp Gln Tyr Glu Glu Phe Cys
 330 335 340
 Phe Ser Val Arg Phe Lys Ala Tyr Pro Gln Ile Arg Cys Thr Trp Thr
 345 350 355
 Phe Ser Arg Lys Ser Phe Pro Cys Glu Gln Lys Gly Leu Asp Asn Gly
 360 365 370
 Tyr Ser Ile Ser Lys Phe Cys Asn His Lys His Gln Pro Gly Glu Tyr
 375 380 385
 Ile Phe His Ala Glu Asn Asp Ala Gln Phe Thr Lys Met Phe Thr
 390 395 400 405
 Leu Asn Ile Arg Arg Lys Pro Gln Val Leu Ala Glu Ala Ser Ala Ser
 410 415 420
 Gln Ala Ser Cys Phe Ser Asp Gly Tyr Pro Leu Pro Ser Trp Thr Trp
 425 430 435
 Lys Lys Cys Ser Asp Lys Ser Pro Asn Cys Thr Glu Glu Ile Thr Glu
 440 445 450
 Gly Val Trp Asn Arg Lys Ala Asn Arg Lys Val Phe Gly Gln Trp Val
 455 460 465

Ser Ser Ser Thr Leu Asn Met Ser Glu Ala Ile Lys Gly Phe Leu Val
 470 475 480 485
 Lys Cys Cys Ala Tyr Asn Ser Leu Gly Thr Ser Cys Glu Thr Ile Leu
 490 495 500
 Leu Asn Ser Pro Gly Pro Phe Ile Glu Asp Asn Ile Ser Phe
 505 510 515
 Tyr Ala Thr Ile Gly Val Cys Leu Leu Phe Ile Val Val Leu Thr Leu
 520 525 530
 Leu Ile Cys His Lys Tyr Lys Lys Glu Phe Arg Tyr Glu Ser Gln Leu
 535 540 545
 Gln Met Val Gln Val Thr Gly Ser Ser Asp Asn Glu Tyr Phe Tyr Val
 550 555 560 565
 Asp Phe Arg Glu Tyr Glu Tyr Asp Leu Lys Trp Glu Phe Pro Arg Glu
 570 575 580
 Asn Leu Glu Phe Gly Lys Val Leu Gly Ser Gly Ala Phe Gly Lys Val
 585 590 595
 Met Asn Ala Thr Ala Tyr Gly Ile Ser Lys Thr Gly Val Ser Ile Gln
 600 605 610
 Val Ala Val Lys Met Leu Lys Glu Lys Ala Asp Ser Ser Glu Arg Glu
 615 620 625
 Ala Leu Met Ser Glu Leu Lys Met Met Thr Gln Leu Gly Ser His Glu
 630 635 640 645
 Asn Ile Val Asn Leu Leu Gly Ala Cys Thr Leu Ser Gly Pro Ile Tyr
 650 655 660

Leu Ile Phe Glu Tyr Cys Cys Tyr Gly Asp Leu Leu Asn Tyr Leu Arg
 665 670 675
 Ser Lys Arg Glu Lys Phe His Arg Thr Trp Thr Glu Ile Phe Lys Glu
 680 685 690
 His Asn Phe Ser Phe Tyr Pro Thr Phe Gln Ser His Pro Asn Ser Ser
 695 700 705
 Met Pro Gly Ser Arg Glu Val Gln Ile His Pro Asp Ser Asp Gln Ile
 710 715 720 725
 Ser Gly Leu His Gly Asn Ser Phe His Ser Glu Asp Glu Ile Glu Tyr
 730 735 740
 Glu Asn Gln Lys Arg Leu Glu Glu Glu Asp Leu Asn Val Leu Thr
 745 750 755
 Phe Glu Asp Leu Leu Cys Phe Ala Tyr Gln Val Ala Lys Gly Met Glu
 760 765 770
 phe Leu Glu Phe Lys Ser Cys Val His Arg Asp Leu Ala Ala Arg Asn
 775 780 785
 Val Leu Val Thr His Gly Lys Val Val Lys Ile Cys Asp Phe Gly Leu
 790 795 800
 Ala Arg Asp Ile Met Ser Asp Ser Asn Tyr Val Val Arg Gly Asn Ala
 810 815 820
 Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ser Leu Phe Glu Gly Ile
 825 830 835
 Tyr Thr Ile Lys Ser Asp Val Trp Ser Tyr Gly Ile Leu Leu Trp Glu
 840 845 850

Ile Phe Ser Leu Gly Val Asn Pro Tyr Pro Gly Ile Pro Val Asp Ala
855 860

Asn Phe Tyr Lys Leu Ile Gln Asn Gly Phe Lys Met Asp Gln Pro Phe
870 875 880

Tyr Ala Thr Glu Glu Ile Tyr Ile Ile Met Gln Ser Cys Trp Ala Phe
890 895 900

Asp Ser Arg Lys Arg Pro Ser Phe Pro Asn Leu Thr Ser Phe Leu Gly
905 910

Cys Gln Leu Ala Asp Ala Glu Glu Ala Met Tyr Gln Asn Val Asp Gly
920 925 930

Arg Val Ser Glu Cys Pro His Thr Tyr Gln Asn Arg Arg Pro Phe Ser
935 940 945

Arg Glu Met Asp Leu Gly Leu Leu Ser Pro Gln Ala Gln Val Glu Asp
950 955 960

Ser

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 208..4311

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 265..4308

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 208..264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTGTGTCCCG CAGCCGGATA ACCTGGCTGA CCCGATTCCG CGGACACCCG TGCAGCCGCG	60
GCTGGAGCCA GGGCGCCGGT GCCCGCGCTC TCCCGGGTCT TCGCGTGGCG GGGCCGATAC	120
CGCCTCTGTG ACTTCTTTGC GGGCCAGGGA CGGAGAAGGA GTCTGTGCCT GAGAAACTGG	180
GCTCTGTGCC CAGGCGCGAG GTGCAGG ATG GAG AGC AAG GGC CTG CTA GCT	231
Met Glu Ser Lys Gly Leu Ala	
-19 -15	
GTC GCT CTG TGG TTC TGC GTG GAG ACC CGA GCC GCC TCT GTG GGT TTG	279
Val Ala Leu Trp Phe Cys Val Glu Thr Arg Ala Ala Ser Val Gly Leu	
-10 -5 1 5	
CCT GGC GAT TTT CTC CAT CCC CCC AAG CTC AGC ACA CAG AAA GAC ATA	327
Pro Gly Asp Phe Leu His Pro Pro Lys Leu Ser Thr Gln Lys Asp Ile	
10 15 20	

CTG ACA ATT TTG GCA AAT ACA ACC CTT CAG ATT ACT TGC AGG GGA CAG Leu Thr Ile Leu Ala Asn Thr Thr Leu Gln Ile Thr Cys Arg Gly Gln 25 30 35	375
CGG GAC CTG GAC TGG CTT TGG CCC AAT GCT CAG CGT GAT TCT GAG GAA Arg Asp Leu Asp Trp Leu Trp Trp Pro Asn Ala Gln Arg Asp Ser Glu Glu 40 45 50	423
AGG GTA TTG GTG ACT GAA TGC GGC GGT GAC AGT ATC TTC TGC AAA Arg Val Leu Val Thr Glu Cys Gly Gly Asp Ser Ile Phe Cys Lys 55 60 65	471
ACA CTC ACC ATT CCC AGG GTG GGT GGA AAT GAT ACT GGA GCC TAC AAG Thr Leu Thr Ile Pro Arg Val Val Gly Asn Asp Thr Gly Ala Tyr Lys 70 75 80 85	519
TGC TCG TAC CGG GAC GTC GAC ATA GCC TCC ACT GTT TAT GTC TAT GTT Cys Ser Tyr Arg Asp Val Asp Ile Ala Ser Thr Val Tyr Val Tyr Val 90 95 100	567
CGA GAT TAC AGA TCA CCA TTC ATC GCC TCT GTC AGT GAC CAG CAT GGC Arg Asp Tyr Arg Ser Pro Phe Ile Ala Ser Val Ser Asp Gln His Gly 105 110 115	615
ATC GTG TAC ATC ACC GAG AAC AAG AAC AAA ACT GTG GTG ATC CCC TGC Ile Val Tyr Ile Thr Glu Asn Lys Lys Thr Val Val Ile Pro Cys 120 125 130	663
CGA GGG TCG ATT TCA AAC CTC AAT GTG TCT CTT TGC GCT AGG TAT CCA Arg Gly Ser Ile Ser Asn Leu Asn Val Ser Leu Cys Ala Arg Tyr Pro 135 140 145	711
GAA AAG AGA TTT GTT CCG GAT GGA AAC AGA ATT TCC TGG GAC AGC GAG Glu Lys Arg Phe Val Pro Asp Gly Asn Arg Ile Ser Trp Asp Ser Glu 150 155 160 165	759

ATA GGC TTT ACT CTC CCC AGT TAC ATG ATC AGC TAT GCC GGC ATG GTC Ile Gly Phe Thr Leu Pro Ser Tyr Met 175 170	807
TTC TGT GAG GCA AAG ATC AAT GAT GAA ACC TAT CAG TCT ATC ATG TAC Phe Cys Glu Ala Lys Ile Asn Asp Glu Thr Tyr Gln Ser Ile Met Tyr 185 190	855
ATA GTT GTG GTT GTA GGA TAT AGG ATT TAT GAT GTG ATT CTG AGC CCC Ile Val Val Val Val Gly Tyr Arg Ile Tyr Asp Val Ile Leu Ser Pro 200 205	903
CCG CAT GAA ATT GAG CTA TCT GCC GGA GAA AAA CTT GTC TTA AAT TGT Pro His Glu Ile Glu Leu Ser Ala Gly Glu Lys Leu Val Leu Asn Cys 215 220 225	951
ACA GCG AGA ACA GAG CTC AAT GTG GGG CTT GAT TTC ACC TGG CAC TCT Thr Ala Arg Thr Glu Leu Asn Val Gly Leu Asp Phe Thr Trp His Ser 230 235 240 245	999
CCA CCT TCA AAG TCT CAT CAT AAG AAG ATT GTA AAC CGG GAT GTG AAA Pro Pro Ser Lys Ser His His Lys Lys Ile Val Asn Arg Asp Val Lys 250 255	1047
CCC TTT CCT GGG ACT GTG GCG AAG ATG TTT TTG AGC ACC TTG ACA ATA Pro Phe Pro Gly Thr Val Ala Lys Met Phe Leu Ser Thr Leu Thr Ile 265 270 275	1095
GAA AGT GTG ACC AAG AGT GAC CAA GGG GAA TAC ACC TGT GTA GCG TCC Glu Ser Val Thr Lys Ser Asp Gln Gly Glu Tyr Thr Cys Val Ala Ser 280 285 290	1143
AGT GGA CGG ATG ATC AAG AGA AAT AGA ACA TTT GTC CGA GTT CAC ACA Ser Gly Arg Met Ile Lys Arg Asn Arg Thr Phe Val Arg Val His Thr 295 300 305	1191

AAG CCT TTT ATT GCT TTC GGT AGT GGG ATG AAA TCT TTG GTG GAA GCC Lys Pro Phe Ile Ala Phe 315 310	1239
ACA GTG GGC AGT CAA GTC CGA ATC CCT GTC AAG TAT CTC AGT TAC CCA Thr Val Gly Ser Gln Val 330 330	1287
GCT CCT GAT ATC AAA TGG TAC AGA AAT GGA AGG CCC ATT GAG TCC AAC Ala Pro Asp Ile Lys Trp Tyr Arg Asn Gly Arg Pro Ile Glu Ser Asn 345 350	1335
TAC ACA ATG ATG GTT GGC GAT GAA CTC ACC ATC ATG GAA GTG ACT GAA Tyr Thr Met Ile Val Gly Asp 360 360	1383
AGA GAT GCA GGA AAC TAC ACG GTC ATC CTC ACC AAC CCC ATT TCA ATG Arg Asp Ala Gly Asn Tyr 375 375	1431
GAG AAA CAG AGC CAC ATG ATG GTC TCT CTG GTT GTG AAT GTC CCA CCC CAG Glu Lys Gln Ser His Met Val 395 390	1479
ATC GGT GAG AAA GCC TTG ATC TCG CCT ATG GAT TCC TAC CAG TAT GGG Ile Gly Glu Lys Ala Leu 410 410	1527
ACC ATG CAG ACA TTG ACA TGC ACA GTC TAC GCC AAC CCT CCC CTG CAC Thr Met Gln Thr Leu Thr 425 425	1575
CAC ATC CAG TGG TAC TGG CAG CTA GAA GCC TGC TCC TAC AGA CCC His Ile Gln Trp Tyr Trp Gln Leu Glu Ala Cys Ser Tyr Arg Pro 440 450	1623

GGC CAA ACA AGC CCG TAT GCT TGT AAA GAA TGG AGA CAC GTG GAG GAT Gly Gln Thr Ser Pro Tyr Ala Cys Lys Glu Trp Arg His Val Glu Asp 455 460 465	1671
TTC CAG GGG GGA AAC AAG ATC GAA GTC ACC AAA AAC CAA TAT GCC CTG Phe Gln Gly Gly Asn Lys Ile Glu Val Thr Lys Asn Gln Tyr Ala Leu 470 475 480 485	1719
ATT GAA GGA AAA AAC AAA ACT GTA AGT ACG CTG GTC ATC CAA GCT GCC Ile Glu Gly Lys Asn Lys Thr Val Ser Thr Leu Val Ile Gln Ala Ala 490 495 500	1767
AAC GTG TCA GCG TTG TAC AAA TGT GAA GCC ATC AAC AAA GCG GGA CGA Asn Val Ser Ala Leu Tyr Lys Cys Glu Ala Ile Asn Lys Ala Gly Arg 505 510 515	1815
GGA GAG AGG GTC ATC TCC TTC CAT GTG ATC AGG GGT CCT GAA ATT ACT Gly Glu Arg Val Ile Ser Phe His Val Ile Arg Gly Pro Glu Ile Thr 520 525 530	1863
GTG CAA CCT GCT GCC CAG CCA ACT GAG CAG GAG AGT GTG TCC CTG TTG Val Gln Pro Ala Ala Gln Pro Thr Glu Gln Glu Ser Val Ser Leu Leu 535 540 545	1911
TGC ACT GCA GAC AGA AAT ACG TTT GAG AAC CTC ACG TGG TAC AAG CTT Cys Thr Ala Asp Arg Asn Thr Phe Glu Asn Leu Thr Trp Tyr Lys Leu 550 555 560 565	1959
GGC TCA CAG GCA ACA TCG GTC CAC ATG GGC GAA TCA CTC ACA CCA GTT Gly Ser Gln Ala Thr Ser Val His Met Gly Glu Ser Leu Thr Pro Val 570 575 580	2007
TGC AAG AAC TTG GAT GCT CTT TGG AAA CTG AAT GGC ACC ATG TTT TCT Cys Lys Asn Leu Asp Ala Leu Trp Lys Leu Asn Gly Thr Met Phe Ser 585 590 595	2055

AAC AGC ACA AAT GAC ATC TTG ATT GTG GCA TTT CAG AAT GCC TCT CTG Asn Ser 600 Thr Asn Asp Ile Leu 605 Ile Val Ala Phe Gln Asn Ala Ser Leu 610	2103
CAG GAC CAA GGC GAC TAT GTT TGC TCT GCT CAA GAT AAG AAG ACC AAG Gln Asp 615 Gln Gly Asp Tyr 620 Val Cys Ser Ala Gln Asp Lys Lys Thr Lys 625	2151
AAA AGA CAT TGC CTG GTC AAA CAG CTC ATC CTA GAG CGC ATG GCA Lys Arg His Cys Leu 635 Val Lys Gln Leu Ile 640 Ile Leu Glu Arg Met Ala 645	2199
CCC ATG ATC ACC GGA AAT CTG GAG AAT CAG ACA ACA ACC ATT GGC GAG Pro Met Ile Thr 650 Gly Asn Leu Glu Asn Gln Thr Thr Ile Gly Glu 660	2247
ACC ATT GAA GTG ACT TGC CCA GCA TCT GGA AAT CCT ACC CCA CAC ATT Thr Ile Glu Val Thr Cys Pro Ala Ser Gly Asn Pro Thr 675 Pro His Ile 670	2295
ACA TGG TTC AAA GAC AAC GAG ACC CTG GTA GAA GAT TCA GGC ATT GTA Thr Trp Phe Lys Asp Asn Glu Thr Leu Val Glu Asp Ser Gly Ile Val 690	2343
CTG AGA GAT GGG AAC CGG AAC CTG ACT ATC CGC AGG GTG AGG AAG GAG Leu Arg Asp Gly Asn Arg 700 Thr Ile Arg Arg Val Arg Lys Glu 705	2391
GAT GGA GGC CTC TAC ACC TGC CAG GCC TGC AAT GTC CTT GGC TGT GCA Asp Gly Gly Leu Tyr 715 Thr Cys Gln Ala Cys Asn Val Leu Gly Cys Ala 720	2439
AGA GCG GAG ACG CTC TTC ATA GAA GGT GCC CAG GAA AAG ACC AAC Arg Ala Glu Thr Leu Phe 730 Ile Ile Glu Gly Ala Gln Glu Lys Thr Asn 740	2487

TTG GAA GTC ATT ATC CTC GTC GGC ACT GCA GTG ATT GCC ATG TTC TTC 2535
 Leu Glu Val Ile Ile Leu Val Gly Thr Ala Val Ile Ala Met Phe Phe
 745 750

 TGG CTC CTT CTT GTC ATT CTC GTA CGG ACC GTT AAG CGG GCC AAT GAA 2583
 Trp Leu Leu Val Ile Leu Val Arg Thr Val Lys Arg Ala Asn Glu
 760 765 770

 GGG GAA CTG AAG ACA GGC TAC TTG TCT ATT GTC ATG GAT CCA GAT GAA 2631
 Gly Glu Leu Lys Thr Gly Tyr Leu Ser Ile Val Met Asp Pro Asp Glu
 775 780 785

 TTG CCC TTG GAT GAG CGC TGT GAA CGC TTG CCT TAT GAT GCC AGC AAG 2679
 Leu Pro Leu Asp Glu Arg Cys Glu Arg Leu Pro Tyr Asp Ala Ser Lys
 790 795 800

 TGG GAA TTC CCC AGG GAC CGG CTG AAA CTA GGA AAA CCT CTT GGC CGC 2727
 Trp Glu Phe Pro Arg Asp Arg Leu Lys Leu Gly Lys Pro Leu Gly Arg
 810 815 820

 GGT GCC TTC GGC CAA GTG ATT GAG GCA GAC GCT TTT GGA ATT GAC AAG 2775
 Gly Ala Phe Gly Gln Val Ile Glu Ala Asp Ala Phe Gly Ile Asp Lys
 825 830 835

 ACA GCG ACT TGC AAA ACA GTA GCC GTC AAG ATG TTG AAA GAA GGA GCA 2823
 Thr Ala Thr Cys Lys Thr Val Ala Val Lys Met Leu Lys Glu Gly Ala
 840 845 850

 ACA CAC AGC GAG CAT CGA GCC CTC ATG TCT GAA CTC AAG ATC CTC ATC 2871
 Thr His Ser Glu His Arg Ala Leu Met Ser Glu Leu Lys Ile Leu Ile
 855 860 865

 CAC ATT GGT CAC CAT CTC AAT GTG GTG AAC CTC CTA GGC GCC TGC ACC 2919
 His Ile Gly His His Leu Asn Val Val Asn Leu Leu Gly Ala Cys Thr
 870 875 880 885

AAG CCG GGA GGG CCT CTC ATG GTG ATT GTG GAA TTC TCG AAG TTT GGA Lys Pro Gly Gly Pro Leu Met Val Ile Val Ile 895 890	2967
AAC CTA TCA ACT TAC TTA CGG GGC AAG AGA AAT GAA TTT GTT CCC TAT Asn Leu Ser Thr Tyr Leu Arg Gly Lys Arg Asn Glu Phe Val Pro Tyr 905 910	3015
AAG AGC AAA GGG GCA CGC TTC CGC CAG GGC AAG GAC TAC GTT GGG GAG Lys Ser Lys Gly Ala Arg Phe Arg Gln Gly Lys Asp Tyr Val Gly Glu 920 930	3063
CTC TCC GTG GAT CTG AAA AGA CGC TTG GAC AGC ATC ACC AGC AGC CAG Leu Ser Val Asp Leu Lys Arg Arg Leu Asp Ser Ile Thr Ser Ser Gln 935 940	3111
AGC TCT GCC AGC TCA GGC TTT GTT GAG GAG AAA TCG CTC AGT GAT GTA Ser Ser Ala Ser Ser Gly Phe Val Glu Glu Lys Ser Leu Ser Asp Val 950 955	3159
GAG GAA GAA GAA GCT TCT GAA GAA CTG TAC AAG GAC TTC CTG ACC TTG Glu Glu Glu Glu Ala Ser Glu Glu Leu Tyr Lys Asp Phe Leu Thr Leu 970 975	3207
GAG CAT CTC ATC TGT TAC AGC TTC CAA GTG GCT AAG GGC ATG GAG TTC Glu His Leu Ile Cys Tyr Ser Phe Gln Val Ala Lys Gly Met Glu Phe 985 990	3255
TTG GCA TCA AGG AAG TGT ATC CAC AGG GAC CTG GCA GCA CGA AAC ATT Leu Ala Ser Arg Lys Cys Ile His Arg Asp Leu Ala Ala Arg Asn Ile 1000 1005 1010	3303
CTC CTA TCG GAG AAG AAT GTG GTT AAG ATC TGT GAC TTC GGC TTG GCC Leu Leu Ser Ser Glu Lys Asn Val Val Lys Ile Cys Asp Phe Gly Leu Ala 1015 1020 1025	3351

CGG GAC ATT TAT AAA GAC CCG GAT TAT GTC AGA AAA GGA GAT GCC CGA 3399
 Arg Asp Ile Tyr Lys Asp Pro Asp Tyr Val Arg Lys Gly Asp Ala Arg 1045
 1030 1035

CTC CCT TTG AAG TGG ATG GCC CCG GAA ACC ATT TTT GAC AGA GTA TAC 3447
 Leu Pro Leu Lys Trp Met Ala Pro Glu Thr Ile Phe Asp Arg Val Tyr 1060
 1050

ACA ATT CAG AGC GAT GTG TGG TCT TTC GGT GTG TTG CTC TGG GAA ATA 3495
 Thr Ile Gln Ser Asp Val Trp Ser Phe Gly Val Leu Trp Glu Ile 1075
 1065

TTT TCC TTA GGT GCC TCC CCA TAC CCT GGG GTC AAG ATT GAT GAA GAA 3543
 Phe Ser Leu Gly Ala Ser Pro Tyr Pro Gly Val Lys Ile Asp Glu Glu 1090
 1080

TTT TGT AGG AGA TTG AAA GAA GGA ACT AGA ATG CGG GCT CCT GAC TAC 3591
 Phe Cys Arg Arg Leu Lys Glu Gly Thr Arg Met Arg Ala Pro Asp Tyr 1105
 1095 1100

ACT ACC CCA GAA ATG TAC CAG ACC ATG CTG GAC TGC TGG CAT GAG GAC 3639
 Thr Thr Pro Pro Glu Met Tyr Gln Thr Met Leu Asp Cys Trp His Glu Asp 1125
 1110 1115

CCC AAC CAG AGA CCC TCG TTT TCA GAG TTG GTG GAG CAT TTG GGA AAC 3687
 Pro Asn Gln Arg Pro Ser Phe Ser Glu Leu Val Glu His Leu Gly Asn 1140
 1130

CTC CTG CAA GCA AAT GCG CAG CAG GAT GGC AAA GAC TAT ATT GTT CTT 3735
 Leu Leu Gln Ala Asn Ala Gln Gln Asp Gly Lys Asp Tyr Ile Val Leu 1155
 1145 1150

CCA ATG TCA GAG ACA CTG AGC ATG GAA GAG GAT TCT GGA CTC TCC CTG 3783
 pro Met Ser Glu Thr Leu Ser Met Glu Glu Asp Ser Gly Leu Ser Leu 1170
 1160 1165

CCT ACC TCA CCT GTT TCC TGT ATG GAG GAA GAG GAA GTG TGC GAC CCC Pro Thr Ser Pro Val Ser 1175 1180	3831
AAA TTC CAT TAT GAC AAC ACA GCA GGA ATC AGT CAT TAT CTC CAG AAC Lys Phe His Tyr Asp Asn Thr Ala Gly Ile Ser His Tyr Leu Gln Asn 1190 1195 1200	3879
AGT AAG CGA AAG AGC CGG CCA GTG AGT GTA AAA ACA TTT GAA GAT ATC Ser Lys Arg Lys Ser Arg Pro Val Ser Val Lys Thr Phe Glu Asp Ile 1210 1215	3927
CCA TTG GAG GAA CCA GAA GTA AAA GTG ATC CCA GAT GAC AGC CAG ACA Pro Leu Glu Glu Pro Glu Val Lys Val Ile Pro Asp Asp Ser Gln Thr 1225 1230	3975
GAC AGT GGG ATG GTC CTT GCA TCA GAA GAG CTG AAA ACT CTG GAA GAC Asp Ser Gly Met Val Leu Ala Ser Glu Glu Leu Lys Thr Leu Glu Asp 1240 1245	4023
AGG AAC AAA TTA TCT CCA TCT TTT GGT GGA ATG ATG CCC AGT AAA AGC Arg Asn Lys Leu Ser Pro Ser Phe Gly Gly Met Met pro Ser Lys Ser 1255 1260	4071
AGG GAG TCT GTG GCC TCG GAA GGC TCC AAC CAG ACC AGT GGC TAC CAG Arg Glu Ser Val Ala Ser Glu Gly Ser Asn Gln Thr Ser Gly Tyr Gln 1270 1275	4119
TCT GGG TAT CAC TCA GAT GAC ACA GAC ACC ACC GTG TAC TCC AGC GAC Ser Gly Tyr His Ser Asp Asp Thr Asp Thr Thr Val Tyr Ser Ser Asp 1290 1295 1300	4167
GAG GCA GGA CTT TTA AAG ATG GTG GAT GCT GCA GTT CAC GCT GAC TCA Glu Ala Gly Leu Leu Lys Met Val Asp Ala Ala Val His Ala Asp Ser 1305 1310 1315	4215

GGG ACC ACA CTG CAG CTC ACC TCC TGT TTA AAT GGA AGT GGT CCT GTC	4263
Gly Thr Thr Leu Gln Leu Thr Ser Cys Leu Asn Gly Ser Gly Pro Val	
1320	1330
CCG GCT CCG CCC CCA ACT CCT GGA AAT CAC GAG AGA GGT GCT GCT TAGATTTTCA	4318
Pro Ala Pro Pro Thr Pro Gly Asn His Glu Arg Gly Ala Ala	
1335	1345
AGTGTGTGTTC TTTCACCCAC CCGGAAGTAG CCACATTTGA TTTTCATTTT TGGAGGAGGG	4378
ACCTCAGACT GCAAGGAGCT TGTCTCTCAGG GCATTTCCAG AGAAGATGCC CATGACCCAA	4438
GAA TGTTGTG ACTCTACTCT CTTTTCCTCAT TATTAAAG TCCTATATAA TGTGCCCTGC	4498
TGTGGTCTCA CTACCAGTTA AAGCAAAAGA CTTTCAAACA CGTGGACTCT GTCCCTCCAAG	4558
AAGTGGCAAC GGCACCTCTG TGAAACTGGA TCGAATGGG AATGCTTTGT GTGTGAGGA	4618
TGGGTGAGAT GTCCCAGGGC CGAGTCTGTC TACCTTGGAG GCTTTGTGGA GGATGCGGCT	4678
ATGAGCCAAG TGTTAAGTGT GGGATGTGGA CTGGGAGGAA GGAAGGCGCA AGCCGTCCGG	4738
AGAGCGGTTG GAGCCTGCAG ATGCATTTGT CTGGCTCTGG TGGAGGTGGG CTTGTGGCCT	4798
GTCAGGAAAC GCAAAGGCGG CCGGCAGGGT TTGGTTTTGG AAGTTTGGG TGCTCTTCAC	4858
AGTCGGGTTA CAGGCGAGTT CCTGTGGCG TTTCTCTACTC CTAATGAGAG TTCTTCCGG	4918
ACTCTTACGT GTCTCTCTGGC CTGGCCCCCAG GAAGGAAATG ATGCAGCTTG CTCTTCTCTC	4978
ATCTCTCAGG CTGTGCCTTA ATTCAGAACA CCAAAGAGA GGAACGTCGG CAGAGGCTCC	5038
TGACGGGGCC GAAGAATTGT GAGAACAGAA CAGAAACTCA GGGTTTCTGC TGGGTGGAGA	5098
CCCACGTGGC GCCCTGGTGG CAGGTCTGAG GGTTCCTGT CAAGTGGCGG TAAAGGCTCA	5158
GGCTGGGTGT CTTCCTCTAT CTCACCTCCT GTCAGGCCCC CAAGTCCCTCA GTATTTTAGC	5218

TTTGTGGCTT	CCTGATGGCA	GAATAATCTT	AATTGGTTGG	TTTGCTCTCC	AGATAATCAC	5278
TAGCCAGATT	TCGAAATTAC	TTTTTAGCCG	AGTTATGAT	AACATCTACT	GTATCCTTTA	5338
GAATTTTAAC	CTATAAAACT	ATGCTACTG	GTTTCTGCCT	GTGTGCTTAT	GTAAAAAAA	5398
AAAAAAA						5406

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1367 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Glu	Ser	Lys	Gly	Leu	Leu	Ala	Val	Ala	Leu	Trp	Phe	Cys	Val	Glu	-5
-19					-15				-10							
Thr	Arg	Ala	Ala	Ser	Val	Gly	Leu	Pro	Gly	Asp	Phe	Leu	His	Pro	Pro	10
							5									
Lys	Leu	Ser	Thr	Gln	Lys	Asp	Ile	Leu	Thr	Ile	Leu	Ala	Asn	Thr	Thr	25
15							20									
Leu	Gln	Ile	Thr	Cys	Arg	Gly	Gln	Arg	Asp	Leu	Asp	Trp	Leu	Trp	Pro	45
30							35									
Asn	Ala	Gln	Arg	Asp	Ser	Glu	Glu	Arg	Val	Leu	Val	Thr	Glu	Cys	Gly	60
							50									
Gly	Gly	Asp	Ser	Ile	Phe	Cys	Lys	Thr	Leu	Thr	Ile	Pro	Arg	Val	Val	75
							65									
							70									

Gly Asn Asp Thr Gly Ala Tyr Lys Cys Ser Tyr Arg Asp Val Asp Ile	80	85	90
Ala Ser Thr Val Tyr Val Tyr Val Arg Asp Tyr Arg Ser Pro Phe Ile	95	100	105
Ala Ser Val Ser Asp Gln His Gly Ile Val Tyr Ile Thr Glu Asn Lys	110	115	120
Asn Lys Thr Val Val Ile pro Cys Arg Gly Ser Ile Ser Asn Leu Asn	130	135	140
Val Ser Leu Cys Ala Arg Tyr Pro Glu Lys Arg Phe Val Pro Asp Gly	145	150	155
Asn Arg Ile Ser Trp Asp Ser Glu Ile Gly Phe Thr Leu Pro Ser Tyr	160	165	170
Met Ile Ser Tyr Ala Gly Met Val Phe Cys Glu Ala Lys Ile Asn Asp	175	180	185
Glu Thr Tyr Gln Ser Ile Met Tyr Ile Val Val Val Gly Tyr Arg	190	195	200
Ile Tyr Asp Val Ile Leu Ser Pro Pro His Glu Ile Glu Leu Ser Ala	210	215	220
Gly Glu Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val	225	230	235
Gly Leu Asp Phe Thr Trp His Ser Pro Pro Ser Lys Ser His His Lys	240	245	250
Lys Ile Val Asn Arg Asp Val Lys Pro Phe Pro Gly Thr Val Ala Lys	255	260	265

Met Phe Leu Ser Thr Leu Thr Ile Glu Ser Val Thr Lys Ser Asp Gln
270 275 280 285

Gly Glu Tyr Thr Cys Val Ala Ser Ser Gly Arg Met Ile Lys Arg Asn
290 295 300

Arg Thr Phe Val Arg Val His Thr Lys Pro Phe Ile Ala Phe Gly Ser
305 310 315

Gly Met Lys Ser Leu Val Glu Ala Thr Val Gly Ser Gln Val Arg Ile
320 325 330

Pro Val Lys Tyr Leu Ser Tyr Pro Ala Pro Asp Ile Lys Trp Tyr Arg
335 340 345

Asn Gly Arg Pro Ile Glu Ser Asn Tyr Thr Met Ile Val Gly Asp Glu
350 355 360 365

Leu Thr Ile Met Glu Val Thr Glu Arg Asp Ala Gly Asn Tyr Thr Val
370 375 380

Ile Leu Thr Asn Pro Ile Ser Met Glu Lys Gln Ser His Met Val Ser
385 390 395

Leu Val Val Asn Val Pro Pro Gln Ile Gly Glu Lys Ala Leu Ile Ser
400 405 410

Pro Met Asp Ser Tyr Gln Tyr Gly Thr Met Gln Thr Leu Thr Cys Thr
415 420 425

Val Tyr Ala Asn Pro Pro Leu His His Ile Gln Trp Tyr Trp Gln Leu
430 435 440 445

Glu Glu Ala Cys Ser Tyr Arg Pro Gly Gln Thr Ser Pro Tyr Ala Cys
450 455 460

Lys Glu Trp Arg His Val Glu Asp Phe Gln Gly Gly Asn Lys Ile Glu
465 470

Val Thr Lys Asn Gln Tyr Ala Leu Ile Glu Gly Lys Asn Lys Thr Val
480 485 490

Ser Thr Leu Val Ile Gln Ala Ala Asn Val Ser Ala Leu Tyr Lys Cys
495 500 505

Glu Ala Ile Asn Lys Ala Gly Arg Gly Glu Arg Val Ile Ser Phe His
510 515 520 525

Val Ile Arg Gly Pro Glu Ile Thr Val Gln Pro Ala Ala Gln Pro Thr
530 535 540

Glu Gln Glu Ser Val Ser Leu Leu Cys Thr Ala Asp Arg Asn Thr Phe
545 550 555

Glu Asn Leu Thr Trp Tyr Lys Leu Gly Ser Gln Ala Thr Ser Val His
560 565 570

Met Gly Glu Ser Leu Thr Pro Val Cys Lys Asn Leu Asp Ala Leu Trp
575 580 585

Lys Leu Asn Gly Thr Met Phe Ser Ser Asn Ser Thr Asn Asp Ile Leu Ile
590 595 600 605

Val Ala Phe Gln Asn Ala Ser Leu Gln Asp Gln Gly Asp Tyr Val Cys
610 615 620

Ser Ala Gln Asp Lys Lys Thr Lys Lys Arg His Cys Leu Val Lys Gln
625 630 635

Leu Ile Ile Leu Glu Arg Met Ala Pro Met Ile Thr Gly Asn Leu Glu
640 645 650

[illegible]

Val Lys Met Leu Lys Glu Gly Ala Thr His Ser Glu His Arg Ala Leu
850 855 860

Met Ser Glu Leu Lys Ile Leu Ile His Ile Gly His His Leu Asn Val
865 870 875

Val Asn Leu Leu Gly Ala Cys Thr Lys Pro Gly Gly Pro Leu Met Val
880 885 890

Ile Val Glu Phe Ser Lys Phe Gly Asn Leu Ser Thr Tyr Leu Arg Gly
895 900 905

Lys Arg Asn Glu Phe Val Pro Tyr Lys Ser Lys Gly Ala Arg Phe Arg
910 915 920 925

Gln Gly Lys Asp Tyr Val Gly Glu Leu Ser Val Asp Leu Lys Arg Arg
930 935 940

Leu Asp Ser Ile Thr Ser Ser Gln Ser Ser Ala Ser Ser Gly Phe Val
945 950 955

Glu Glu Lys Ser Leu Ser Asp Val Glu Glu Glu Glu Ala Ser Glu Glu
960 965 970

Leu Tyr Lys Asp Phe Leu Thr Leu Glu His Leu Ile Cys Tyr Ser Phe
975 980 985

Gln Val Ala Lys Gly Met Glu Phe Leu Ala Ser Arg Lys Cys Ile His
990 995 1000 1005

Arg Asp Leu Ala Ala Arg Asn Ile Leu Leu Ser Glu Lys Asn Val Val
1010 1015 1020

Lys Ile Cys Asp Phe Gly Leu Ala Arg Asp Ile Tyr Lys Asp Pro Asp
1025 1030 1035

Tyr Val Arg Lys Gly Asp Ala Arg Leu Pro Leu Lys Trp Met Ala Pro
 1040 1045 1050
 Glu Thr Ile Phe Asp Arg Val Tyr Thr Ile Gln Ser Asp Val Trp Ser
 1055 1060 1065
 Phe Gly Val Leu Leu Trp Glu Ile Phe Ser Leu Gly Ala Ser Pro Tyr
 1070 1075 1080 1085
 Pro Gly Val Lys Ile Asp Glu Glu Phe Cys Arg Arg Leu Lys Glu Gly
 1090 1095 1100
 Thr Arg Met Arg Ala Pro Asp Tyr Thr Thr Pro Glu Met Tyr Gln Thr
 1105 1110 1115
 Met Leu Asp Cys Trp His Glu Asp Pro Asn Gln Arg Pro Ser Phe Ser
 1120 1125 1130
 Glu Leu Val Glu His Leu Gly Asn Leu Leu Gln Ala Asn Ala Gln Gln
 1135 1140 1145
 Asp Gly Lys Asp Tyr Ile Val Leu Pro Met Ser Glu Thr Leu Ser Met
 1150 1155 1160 1165
 Glu Glu Asp Ser Gly Leu Ser Leu Pro Thr Ser Pro Val Ser Cys Met
 1170 1175 1180
 Glu Glu Glu Glu Val Cys Asp Pro Lys Phe His Tyr Asp Asn Thr Ala
 1185 1190 1195
 Gly Ile Ser His Tyr Leu Leu Gln Asn Ser Lys Arg Lys Ser Arg Pro Val
 1200 1205 1210
 Ser Val Lys Thr Phe Glu Asp Ile Pro Leu Glu Glu Pro Glu Val Lys
 1215 1220 1225

TELE 20 " BOUT 560

Val Ile Pro Asp Asp Ser Gln Thr Asp Ser Gly Met Val Leu Ala Ser 1230 1235 1240 1245
 Glu Glu Leu Lys Thr Leu Glu Asp Arg Asn Lys Leu Ser Pro Ser Phe 1250 1255 1260
 Gly Gly Met Met Pro Ser Lys Ser Arg Glu Ser Val Ala Ser Glu Gly 1265 1270 1275
 Ser Asn Gln Thr Ser Gly Tyr Gln Ser Gly Tyr His Ser Asp Asp Thr 1280 1285 1290
 Asp Thr Thr Val Tyr Ser Ser Asp Glu Ala Gly Leu Leu Lys Met Val 1295 1300 1305
 Asp Ala Ala Val His Ala Asp Ser Gly Thr Thr Leu Gln Leu Thr Ser 1310 1315 1320 1325
 Cys Leu Asn Gly Ser Gly Pro Val Pro Ala Pro Pro Thr Pro Gly 1330 1335 1340
 Asn His Glu Arg Gly Ala Ala 1345

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AATTCGTGCA CTTTCTGTCA CCATGAGTGC ACTTCTGATC CTAGCCCTTG TGGGAGCTGC 60

TGTTGCTGAC TACAAAGATG ATGATGACAA GATCTA 96

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AGCTTAGATC TTGTCATCAT CATCTTTGTA GTCAGCAACA GCAGCTCCCA CAGAGGCTAG 60

GATCAGAAGT GCATCATGG TGACAGAAAG TCGACG 96

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGAGAAGATC TCAAACCAAG ACCTGCCTGT

30

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCAATGGCGG CCGCTCAGGA GATGTTGTCT TGGA

34